

## 21.11 DOPING

DOPING specifies doping profiles either analytically or from an input file. The alias for this parameter is PROFILE.

### Syntax

```
DOPING <prof> [<psp>] [<bound>] [<loc>] [<sprea>>] [OUTFILE=<fn>] [<trps>]
```

Parameter	Type	Default	Units
1D.PROC	Logical	False	
2D.ASCII	Logical	False	
A.MAX	Real	360.0	Degrees
A.MIN	Real	0.0	Degrees
ACCEPTOR	Logical	False	
ACTIVE	Logical	True	
ALUMINUM	Logical	False	
ANTIMONY	Logical	False	
ARSENIC	Logical	False	
ASCII	Logical	False	
ASPECT.RATIO	Logical		
ATHENA	Logical	False	
ATHENA.1D	Logical	False	
BACKDOPE	Real	none	cm <sup>-3</sup>
BORON	Logical	False	
C.MULT	Real	1.0	
CHARACTERISTIC	Real		µm
CHEMICAL	Logical	False	
CONCENTRATION	Real	0	cm <sup>-3</sup>
DEGEN.FAC	Real		
DEVICE	Character		1
DIRECTION	Character	y	
DONOR	Logical	False	

Parameter	Type	Default	Units
DOP.OFFSET	Real	0	cm <sup>-3</sup>
DOP.SEED	Integer	-10	
DOP.SIGMA	Real	0.0	cm <sup>-3</sup>
DOP.XMIN	Real		
DOP.XMAX	Real		
DOP.YMIN	Real		
DOP.YMAX	Real		
DOSE	Real		cm <sup>-2</sup>
ERFC	Logical	False	
ERFC.LATERAL	Logical	False	
E.LEVEL	Real		eV
F.COMPOSIT	Character		
F.DOPING	Character		
F3.DOPING	Character		
FILE	Character		
GAUSSIAN	Logical	False	
IMATER	Character	None	
IN.FILE	Character		
INDIUM	Logical	False	
INFILE	Character		
INAME	Character	None	
INT.LIN	Logical	False	
INT.LOG	Logical	True	
INT.OPTM	Logical	False	
IREGION	Character	None	
JUNCTION	Real		µm
LAT.CHAR	Real		µm
MASTER	Logical	False	
MATERIAL	Character		

Parameter	Type	Default	Units
METAL	Logical	False	
N.COLUMN	Integer		
N.TYPE	Logical	False	
N-TYPE	Logical	False	
N.OFFSET	Real	0.0	cm <sup>-3</sup>
N.PEAK	Real	0	cm <sup>-3</sup>
NAME	Character		
NET	Logical	False	
NOROLLOFF	Logical	False	
NOXROLLOFF	Logical	False	
NOYROLLOFF	Logical	False	
NOZROLLOFF	Logical	False	
OUTFILE	Character		
OUTSIDE	Logical	False	
OX.CHARGE	Logical	False	
PEAK	Real		
PHOSPHORUS	Logical	False	
P.COLUMN	Integer		
P.TYPE	Logical	False	
P-TYPE	Logical	False	
R.MAX	Real	Device Radius	µm
R.MIN	Real	0.0	µm
RATIO.LATERAL	Real	0.7	
RESISTI	Real		Ω·cm
REGION	Integer	All	
SIGN	Real		cm <sup>2</sup>
SIGP	Real		cm <sup>2</sup>
SLICE.LAT	Real		µm
SPECIES1	Logical	False	

Parameter	Type	Default	Units
SPECIES2	Logical	False	
SPECIES3	Logical	False	
START	Real	0	
STRUCTURE	Character		
SUPREM3	Logical	False	
TMA.SUPREM3	Logical	False	
TAT.TRAP	Logical	False	
TAUN	Real		
TAUP	Real		
TRAP	Logical	False	
UNIFORM	Logical	False	
WIDTH	Real	width of structure	µm
X1	Real	0	µm
X2	Real	0	µm
XY	Logical	True	
XZ	Logical	False	
X.CHAR	Real		µm
X.COLUMN	Integer		
X.COMP	Logical	False	
X.DIR	Logical	False	
X.ERFC	Logical	False	
X.FLIP	Logical	False	
X.LEFT	Real	left of structure	µm
X.MAX	Real		µm
X.MIN	Real		µm
X.SCALE	Logical	True	
X.RIGHT	Real	right of structure	µm
XERFC.LAT	Logical	False	
XY.RATIO	Real	0.7	

Parameter	Type	Default	Units
Y.BOTTOM	Real	bottom of structure	µm
Y.CHAR	Real		µm
Y.COLUMN	Integer		
Y.FLIP	Logical	False	
Y.JUNCTI	Real		µm
Y1	Real	0	µm
Y2	Real	0	µm
YX	Logical	True	
YZ	Logical	False	
Y.COMP	Logical	False	
Y.DIR	Logical	False	
Y.MAX	Real		µm
Y.MIN	Real		µm
Y.SCALE	Logical	True	
Y.TOP	Real	top of structure	
Z1	Real	0	µm
Z2	Real	0	µm
ZY	Logical	False	
ZX	Logical	False	
Z.BACK	Real		
Z.DIR	Logical	False	
Z.FRONT	Real		
Z.MAX	Real		µm
Z.MIN	Real		µm
Z.SCALE	Logical	True	
ZERFC.LAT	Logical	False	
ZLAT.CHAR	Real		
ZRATIO.LAT	Real	0.7	
ZSLICE.LAT	Real		

## Description

The DOPING statement is used to define doping profiles in the device structure. Typically a sequence of DOPING statements is given each building on the others.

<b>OUTFILE</b>	Specifies the name of an output file for use with REGRID. The first DOPING statement should use this parameter to specify a filename. All doping information from the first DOPING statement and all subsequent DOPING statements in the input file are saved to this file. The REGRID statement can read this file and interpolate doping on the new grid.
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**Note:** The file from OUTFILE cannot be used in TONYPLOT or in the MESH statement. The SAVE command should be used after all of the DOPING commands required to save a file for plotting the doping profile.

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## Statement Applicability Parameters

<b>DEVICE</b>	Specifies which device the statement applies to in the MIXEDMODE simulation. The synonym for this parameter is STRUCTURE.
<b>MATERIAL</b>	Restricts the applicability of the statement to regions of the specified material.
<b>NAME</b>	Restricts the applicability of the statement to regions with the specified name.
<b>REGION</b>	Restricts the applicability of the statement to regions with the specified region number.
<b>STRUCTURE</b>	This is a synonym for DEVICE.

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**Note:** If you don't specify the DEVICE, MATERIAL, NAME and REGION parameters, the DOPING statement will apply to all regions.

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## Interface Doping Profile Location Parameters

You can use these parameters with the parameters NAME, MATER, and REGION to describe interfaces between regions to be doped with an analytic profile. The NAME, MATER, and REGION parameters are used to describe the regions that receive the doping while the INAME, IMATER, and IREGION parameters describe regions incident on the regions receiving the doping where the doping is to be placed (i.e., along the interface).

The locations of these interface profiles may also be restricted by the location parameters X.MAX, X.MIN, Y.MAX, and Y.MIN.

<b>IMATER</b>	Specifies the material of all neighboring regions where an interface profile is placed.
<b>INAME</b>	Specifies the name of a neighboring region where an interface profile is placed.
<b>IREGION</b>	Specifies the region number of the a neighboring region where the interface profile is placed.
<b>OUTSIDE</b>	Specifies that interface regions will placed at all interfaces with the outside of the simulation domain.

## Analytical Profile Types

These parameters specify how ATLAS will generate a doping profile from analytical functions.

<b>DOP.SIGMA</b>	Specifies the variance for random gaussian dopant distribution.
<b>DOP.SEED</b>	Specifies a seed value for random gaussian dopant distribution.
<b>ERFC</b>	Specifies the use of a ERFC analytical function to generate the doping profile. If ERFC is specified, the following parameters must also be specified: <ul style="list-style-type: none"> <li>• Polarity parameters N.TYPE or P.TYPE</li> <li>• One of the following groups of profile specifications:               <ul style="list-style-type: none"> <li>• Group 1:CONCENTRATION and JUNCTION</li> <li>• Group 2:DOSE and CHARACTERISTIC</li> <li>• Group 3:CONCENTRATION and CHARACTERISTIC</li> </ul> </li> </ul>
<b>GAUSSIAN</b>	Specifies the use of a gaussian analytical function to generate the doping profile. If GAUSSIAN is specified, the following parameters must also be specified: <ul style="list-style-type: none"> <li>• Polarity parameters N.TYPE or P.TYPE</li> <li>• One of the following groups of profile specifications:               <ul style="list-style-type: none"> <li>• Group 1:CONCENTRATION and JUNCTION</li> <li>• Group 2:DOSE and CHARACTERISTIC</li> <li>• Group 3:CONCENTRATION and CHARACTERISTIC</li> </ul> </li> </ul>

<b>UNIFORM</b>	Specifies the use of uniform (constant) analytical functions to generate the doping profile. If <b>UNIFORM</b> is specified, the <b>N.TYPE</b> , <b>P.TYPE</b> , and <b>CONCENTRATION</b> parameters must be specified. Doping is introduced into a box defined by the boundary parameters (see the “ <a href="#">Boundary Conditions</a> ” on page <a href="#">958</a> ). The box by default includes the entire region.
<b>F.COMPOSIT</b>	Specifies the name of a file containing a C-Interpreter function specifying the spatial distribution of composition fractions.
<b>F.DOPING</b>	Specifies the name of a file containing a C-Interpreter function specifying the spatial distribution of dopants.
<b>F3.DOPING</b>	Specifies the name of a file containing a C-Interpreter function specifying the spatial distribution of dopants for a 3D device.

## File Import Profile Types

These parameters specify how ATLAS will generate a doping profile from a file. Files can be user-defined or from process simulation.

<b>1D.PROC</b>	Specifies is an alias for TMA.SUPREM3.								
<b>2D.ASCII</b>	Specifies that a 2D doping profile, which is defined on a rectangular Cartesian grid, should be loaded from a file specified by <code>INFILE</code> . <b>2D.ASCII</b> must be specified along with either the <code>N.TYPE</code> , <code>P.TYPE</code> or <code>NET</code> parameters. This first column of the file should contain the X coordinates. The second column should contain the Y coordinates. The third column should contain the doping data.								
<b>ASCII</b>	<p>There has two separate meanings. The first meaning is that it specifies the file type as ASCII when it's combined with other format parameters. The second meaning is when this parameter is used alone, it specifies ASCII data files containing concentration versus depth information. The alias for this parameter is <code>1D.PROC</code>.</p> <p>In the second meaning, this parameter must be written in the form:</p> <pre>ASCII INFILE=&lt;filename&gt;</pre> <p>where <code>filename</code> is the name of the ASCII input file. The data file must be in the following format:</p> <table style="margin-left: 200px;"> <tr><td>depth</td><td>concentration</td></tr> <tr><td>depth</td><td>concentration</td></tr> <tr><td>depth</td><td>concentration</td></tr> <tr><td colspan="2">...</td></tr> </table> <p>where <code>depth</code> is specified in <math>\mu\text{m}</math> and <code>concentration</code> is specified in <math>\text{cm}^{-3}</math>. An input file name, a dopant type, and boundary parameters must be specified. Positive concentrations are assumed to be n-type and negative concentrations are assumed to be p-type unless the <code>N.TYPE</code> or <code>P.TYPE</code> parameters are used.</p>	depth	concentration	depth	concentration	depth	concentration	...	
depth	concentration								
depth	concentration								
depth	concentration								
...									
<b>ATHENA.1D</b>	Specifies that the doping file is a ATHENA 1D export file. This parameter acts in a similar way to the <code>SSUPREM3</code> parameter.								
<b>ATHENA</b>	Reads 2D doping information from ATHENA standard structure file (SSF) or PISCES-II format files. The PISCES-II format is an obsolete file format. Doping information obtained from this file will be added to each point of the current ATLAS mesh. If points in the ATLAS mesh do not coincide with points in the ATHENA mesh, doping for ATLAS mesh points will be interpolated from ATHENA doping information. If this profile type is used, the <code>INFILE</code> parameter must also be specified.								

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**Note:** The `X.STRETCH` function available in previous versions of ATLAS has been replaced by similar more powerful functions in `DEVEDIT`. This feature should no longer be used in ATLAS.

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<b>FILE</b>	This is an alias for <code>INFILE</code> .
<b>IN.FILE</b>	This is a synonym for <code>INFILE</code> . The alias for this parameter is <code>FILE</code> .
<b>INFILE</b>	Specifies the name of the appropriate input file. The synonym for this parameter is <code>IN.FILE</code> .
<b>MASTER</b>	Specifies that the <code>INFILE</code> is written in the Silvaco standard structure file (SSF) format. This file format is the default output format of ATHENA and SSUPREM3. This parameter is typically combined with the <code>SSUPREM3</code> , <code>ATHENA 1D</code> , or <code>ATHENA</code> parameters. If neither of these are used the default is <code>SUPREM3</code> .
<b>N.COLUMN</b>	Specifies which column of an 2D ASCII table corresponds to the net donor concentration when <code>2D.ASCII</code> is specified.
<b>P.COLUMN</b>	Specifies which column of an 2D ASCII table corresponds to the net acceptor concentration when <code>2D.ASCII</code> is specified.
<b>SUPREM3</b>	Specifies the <code>INFILE</code> was produced by SSUPREM3 in standard structure file (SSF) format or binary or an ASCII export format. If this profile type is used, an input file name, a dopant, and boundary parameters must be specified. When SSUPREM3 produces an output file, the doping profiles are stored by dopant. Therefore, a dopant parameter should be specified in order to import the correct doping profile into ATLAS. If a specific dopant is not specified the total donors and acceptor concentrations are loaded.
<b>TMA.SUPREM3</b>	Specifies that the file specified by <code>INFILE</code> is in TMA SUPREM3 binary format. The alias for this parameter is <code>1D.PROC</code> .

**Note:** Files containing 1D doping profiles can be loaded into BLAZE, BLAZE3D, DEVICE3D, or S-PISCES. Files containing 2D doping profiles can only be loaded into S-PISCES.

<b>X.COLUMN</b>	Specifies which column of an 2D ASCII table corresponds to the X coordinate value when <code>2D.ASCII</code> is specified.
<b>Y.COLUMN</b>	Specifies which column of an 2D ASCII table corresponds to the Y coordinate value when <code>2D.ASCII</code> is specified.

## 1D Profile Modifications

These parameters are used to modify the concentrations in 1D profiles.

<b>C.MULT</b>	Acts as a multiplier in 1D ASCII dopant profiles.
<b>DOP.OFFSET</b>	Subtracts a background doping value from the ATHENA or SSUPREM3 doping. The alias for this parameter is <code>N.OFFSET</code> .

## Dopant Type Specification Parameters

These parameters give information about the dopant species or type to be used in the specified profile. Different profile types require different profile specifications.

<b>ACTIVE</b>	Specifies that for the dopant specified the active concentration as opposed to the chemical concentration is added. This is true by default. Files from ATHENA or SSUPREM3 contain both active and chemical concentrations for each dopant.
<b>ALUMINUM</b>	Specifies that aluminum dopant information be extracted from an imported file.
<b>ANTIMONY</b>	Specifies that antimony dopant information be extracted from an imported file.
<b>ARSENIC</b>	Specifies that arsenic dopant information be extracted from an imported file.
<b>BORON</b>	Specifies that boron dopant information be extracted from an imported file.
<b>C.MULT</b>	Acts as a multiplier in 1D ASCII dopant profiles.
<b>CHEMICAL</b>	Specifies that the chemical concentration (as opposed to the active concentration) will be read from the imported file. This is generally not advisable.
<b>DOP.OFFSET</b>	Subtracts a background doping value from the ATHENA or SSUPREM3 doping. The alias for this parameter is <b>N.OFFSET</b> .
<b>E.LEVEL</b>	Sets the energy of the discrete trap level. For acceptors, <b>E.LEVEL</b> is relative to the conduction band edge. For donors, it is relative to the valence band edge.
<b>INDIUM</b>	Specifies that indium dopant information be extracted from an imported file.
<b>METAL</b>	Specifies that the DOPING statement will define metal atomic concentration used in calculation of electrode quenching.
<b>NET</b>	Specifies that net doping information be extracted from an imported file. This is usually not advisable. It is better to use several DOPING statements to extract data dopant by dopant from a file.
<b>N.OFFSET</b>	This is an alias for <b>DOP.OFFSET</b> .
<b>N.TYPE, N-TYPE, DONOR</b>	Specifies an n-type or donor dopant. This parameter may be used with GAUSSIAN and UNIFORM profile types.
<b>OX.CHARGE</b>	Specifies a fixed oxide charge profile. Oxide charge can only be placed in any insulator region. The <b>N.TYPE/P.TYPE</b> parameters are not used hence a negative concentration implies a negative charge.
<b>P.TYPE, P-TYPE, ACCEPTOR</b>	Specifies a p-type or acceptor dopant. This parameter may be used with GAUSSIAN and UNIFORM profile types.

<b>PHOSPHORUS</b>	Specifies that phosphorus dopant information be extracted from an imported file.
<b>RESISTI</b>	This can be used to specify resistivity (in units of Ohm.cm) as an alternative to using the CONC parameter. Tabulated values are used to convert from the value of RESISTI to doping Concentration (in units of $\text{cm}^{-3}$ ). The tables are related to the ARORA mobility model at 300K and the result depends on whether the dopant has been specified as a donor or an acceptor. At high doping levels, the resistivity can also depend on the particular dopant species. But this is not taken into account in this model.
<b>SPECIES1</b>	Stipulates that the doping profile is to apply to generic ion species 1.
<b>SPECIES2</b>	Stipulates that the doping profile is to apply to generic ion species 2.
<b>SPECIES3</b>	Stipulates that the doping profile is to apply to generic ion species 3.
<b>TRAP</b>	Specifies that the dopant concentration is to be treated as a trap state density.
<b>X.COMP</b>	Specifies a profile of composition fraction x as defined in <a href="#">Appendix B "Material Systems"</a> . This profile can be used to change the composition fraction of cations in ternary and quaternary materials over a spatial distribution.
<b>Y.COMP</b>	Specifies a profile of composition fraction y as defined in <a href="#">Appendix B "Material Systems"</a> . This profile can be used to change the composition fraction of anions in ternary and quaternary materials over a spatial distribution.

### Vertical Distribution Parameters

<b>CHARACTERISTIC</b>	<p>Specifies the principal characteristic length of the implant. For Gaussians, the characteristic length is equal to the square root of two times the standard deviation. If this parameter is left unspecified, the principal characteristic can be computed from the values of the</p> <ul style="list-style-type: none"> <li>• Polarity Parameters</li> <li>• Boundary Parameters</li> <li>• Concentration and Junction parameters</li> </ul> <p>The alias for this parameter is Y.CHAR.</p>
<b>CONCENTRATION</b>	Specifies the peak concentration when a Gaussian profile is used. If this parameter is not specified, peak concentration may be computed from the values of the polarity, boundary, DOSE, or RESISTI, CHARACTERISTIC concentrations. When a uniform profile is specified, the CONCENTRATION parameter sets the value of the uniform doping level. Concentrations must be positive. The alias for this parameter is N.PEAK.
<b>DOSE</b>	Specifies the total dose for a Gaussian profile.

<b>JUNCTION</b>	Specifies the location of a p-n junction within the silicon region of a Gaussian profile. When JUNCTION is specified, the characteristic length is computed by examining the doping at a point halfway between the end of the constant box and the given depth. The JUNCTION location is evaluated considering all previous DOPING statements only. This means that in some cases the order of DOPING statements is important.
<b>N.PEAK</b>	This is an alias for CONCENTRATION.
<b>PEAK</b>	Specifies the depth location of the peak doping in a Gaussian profile.
<b>Y.CHAR</b>	This is an alias for CHARACTERISTIC. See <a href="#">Equation 21-3</a> .
<b>Y.JUNCTI</b>	This is an alias for JUNCTION. See <a href="#">Equation 21-3</a> .

$$N(Y) = \text{PEAK} \cdot \exp\left[-\left(\frac{Y}{Y.\text{CHAR}}\right)^2\right] \quad 21-3$$

### Location Parameters

<b>DIRECTION</b>	Specifies the axis along which a one-dimensional profile is directed in a two-dimensional device (x or y). DIR=y will typically be used for implanted profiles.
<b>REGION</b>	Specifies the region number where doping is to be added.
<b>START</b>	Specifies the depth in the Y direction where the profile should start.

### Lateral Extent Parameters

These parameters must be specified when a 1D doping profile type is used (MASTER, GAUSSIAN, ASCII, ERFC, or UNIFORM). These boundary parameters set the doping boundaries before applying lateral spreading. This is equivalent to setting implant mask edges.

<b>WIDTH</b>	Specifies the extent of the profile in the X direction. Specifying WIDTH is equivalent to specifying X.MAX such that X.MAX=X.MIN+WIDTH.
<b>R.MIN, R.MAX, A.MIN, and A.MAX</b>	For an ATLAS3D device created using the MESH CYLINDRICAL option, these parameters restrict the radial and angular positions respectively of the analytical doping profile. The principal direction of the analytical doping profile is the Z direction in this case.
<b>X.MIN, X.MAX, Y.MIN, Y.MAX, Z.MAX, and Z.MIN</b>	Specify the x, y and z bounds of a rectangular shaped region or box in the device. The dopant profile within this box will be constant with a density equal to the value specified by the CONC parameter. Outside this box the profile decreases from the peak, CONC, with distance, from the box along the principal axes. The relationship between the concentration, outside the box, to distance will depend upon the profile type as specified by the GAUSSIAN, MASTER, ATHENA, ATLAS, and UNIFORM parameters.
<b>X.LEFT, X.MIN</b>	Specifies the left boundary of a vertical 1D profile.

<b>X.RIGHT, X.MAX</b>	Specifies the right boundary of a vertical 1D profile.
<b>Y.BOTTOM, Y.MAX</b>	Specifies the bottom boundary of a horizontal 1D profile.
<b>Y.TOP, Y.MIN</b>	Specifies the top boundary of a horizontal 1D profile.
<b>Z.BACK, Z.MIN</b>	Specifies the back boundary of a z directed 1D or 2D profile.
<b>Z.FRONT, Z.MAX</b>	Specifies the front boundary of a z directed 1D or 2D profile.

### Lateral Distribution Parameters

These parameters specify how a vertical 1D profile is extended outside the box defined by the lateral extent parameters.

<b>BACKDOPE</b>	Specifies the value to which the doping profile specified from the 1D profile will roll-off to outside its lateral and vertical extents. If this value is not specified, then the last doping value in the ASCII file is used as the background doping level, regardless of windowing in the Y direction. If NOXROLLOFF is used, then BACKDOPE will be ignored for the X direction. If NOYROLLOFF is used, then BACKDOPE will be ignored for the Y direction. If NOROLLOFF is used, then BACKDOPE will be completely ignored.
<b>ERFC.LATERAL</b>	Specifies that the complementary error function will be used to calculate the lateral falloff of doping level in the X direction. If you set the <b>X.DIR</b> flag, then this flag will apply to the Y direction instead. If you set ERFC for the analytical doping profile, then ERFC.LATERAL will be automatically enabled by default. If you set GAUSSIAN or UNIFORM, then ERFC.LATERAL will be disabled by default and the falloff will follow a Gaussian profile. The aliases for this parameter are <b>X.ERFC</b> and <b>XERFC.LAT</b> .
<b>LAT.CHAR</b>	Specifies the characteristic length of the lateral profile. If this parameter is not specified, the characteristic length is defined by:  $CL = RL \times OCL$ 21-4 where: <ul style="list-style-type: none"> <li>• CL is the lateral characteristic length in the X direction.</li> <li>• RL is the value of <b>RATIO.LATERAL</b>.</li> <li>• OCL is the characteristic length of the original profile in the Y direction.</li> </ul> The alias for this parameter is <b>X.CHAR</b> .
<b>NOXROLLOFF</b>	Causes the doping level to abruptly change to zero outside the x-limits.
<b>NOYROLLOFF</b>	Causes the doping level to abruptly change to zero outside the y-limits.
<b>NOROLLOFF</b>	This is the same as setting both NOXROLLOFF and NOYROLLOFF.
<b>NOZROLLOFF</b>	Causes the doping levels to abruptly change to zero outside the z-limits.
<b>RATIO.LATERAL</b>	This is the ratio of characteristic lengths in the X and Y directions.

<b>SLICE.LAT</b>	Specifies the point at which the doping is examined to compute the characteristic length of a Gaussian profile after JUNCTION has been specified. The default for this parameter is a point halfway between the end of the constant box and the given depth.
<b>X.CHAR</b>	This is an alias for LAT.CHAR.
<b>X.ERFC</b>	This is an alias for ERFC.LAT.
<b>XERFC.LAT</b>	This is an alias for ERFC.LAT.
<b>XY.RATIO</b>	This is an alias for RATIO.LATERAL.
<b>ZLAT.CHAR</b>	Specifies the characteristic length of the lateral profile in the Z direction. See also LAT.CHAR.
<b>ZERFC.LAT</b>	Specifies that the complementary error function will be used to calculate the lateral falloff of doping level in the Z direction in ATLAS3D. If you specify ERFC as the analytical doping profile, then ZERFC.LAT will be enabled by default. The parameters ZLAT.CHAR and ZRATIO.LAT control the degree of lateral rolloff in the Z direction.
<b>ZRATIO.LAT</b>	This is used analogously to RATIO.LATERAL but applies to lateral spreading in the Z direction. See also LAT.CHAR.
<b>ZSLICE.LAT</b>	This is similar to SLICE.LAT but applies to profiles in the Z direction.

### Trap Parameters

<b>E.LEVEL</b>	Sets the energy of the discrete trap level. For acceptors, E.LEVEL is relative to the conduction band edge, for donors it is relative to the valence band edge.
<b>DEGEN.FAC</b>	Specifies the degeneracy factor of the trap level used to calculate the density.
<b>SIGN</b>	Specifies the capture cross section of the trap for electrons.
<b>SIGP</b>	Specifies the capture cross section of the trap for holes.
<b>TAT.TRAP</b>	Causes the trap level to be used in the ITAT/RTAT model. The trap must be located in an insulator or wide bandgap semiconductor quantum barrier.
<b>TAUN</b>	Specifies the lifetime of electrons in the trap level.
<b>TAUP</b>	Specifies the lifetime of holes in the trap level.

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**Note:** See Section 21.63 "TRAP" for more information on each of these parameters

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### Angled Distribution Parameters

<b>x1, y1, x2, y2</b>	Specify the X and Y coordinates of the ends of the line segment describing the location of the specified angled profile.
<b>X.DIR and Y.DIR</b>	Specify the direction in which the angled profile is extended.

In DEVICE3D, (see [Chapter 6 “3D Device Simulator”](#) for more information about this simulator), dopants can be added along angled segments in the XY plane. The start and ending coordinates of the line segment are defined by the x1, y1, x2, and y2 parameters. You can then specify whether a 2D profile is extended from the line segment in either the X or the Y direction. To specify it, set the X.DIR or Y.DIR parameter. You can then specify a 2D doping profile in the same DOPING statement. The profile can be an analytic, SUPREM, ASCII, or SUPREM4.

The dopants are placed relative to the defined line segment, according to the setting of X.DIR or Y.DIR. If X.DIR is specified, then the effective Y coordinate of the profile is the device Z coordinate and the effective X coordinate of the profile is the distance in the X direction from the center of the line segment. No dopants are added if the device Y coordinate is outside of the Y coordinates of the line segment. If Y.DIR is specified, then the effective Y coordinate of the profile is the device Z coordinate and the effective X coordinate of the profile is the distance in the Y direction from the center of the line segment. No dopants are added if the device X coordinate is outside the X coordinates of the line segment.

### Analytical Doping Definition Example

This example describes a 1.0 $\mu\text{m}$  n-channel MOSFET using Gaussian source and drain profiles. The lateral extent of the source is given by X.RIGHT=2. This corresponds to the mask edge for the implant. Sub-diffusion is determined by an error function based on the RATIO.LAT and JUNCTION parameters. For both source and drain, the n+ doping is added to the uniform p-well concentration to ensure a junction depth of 0.3 $\mu\text{m}$ .

```
DOP UNIF CONC=1E16 P.TYPE
DOP GAUSS CONC=9E19 N.TYPE X.RIGHT=2 JUNC=0.3 RATIO.LAT=0.6
ERFC.LAT
DOP GAUSS CONC=9E19 N.TYPE X.LEFT=3 JUNC=0.3 RATIO.LAT=0.6
ERFC.LAT
```

### 1D ATHENA or SSUPREM3 Interface Example

This example reads a 1D ATHENA bipolar profile and adds it to a uniform substrate concentration. The base and emitter doping are loaded from the same file by specifying the impurity required for each area (boron in the base and arsenic in the emitter).

The DOPOFF parameter is used to subtract the substrate arsenic dopant out of the 1D profile that is loaded since this dopant was already specified in the substrate doping line.

Versions of SSUPREM3 later than 5.0 use standard structure files as default when saving data. These can be loaded in ATLAS with the syntax below by replacing ATHENA.1D with SSUPREM3.

```
# SUBSTRATE
DOP REGION=1 UNIF CONC=1E16 N.TYPE
# BASE
```

```
DOP REGION=1 MASTER ATHENA.1D BORON RATIO.LAT=0.7 INF=bipolar.exp  
#    EMITTER  
DOP REGION=1 MASTER ATHENA.1D ARSENIC RATIO.LAT=0.6 \  
INF=bipolar.exp X.LEFT=12.0 X.RIGHT=13.0 DOPOFF=1e16
```

### Athena Doping Interface Example

This example demonstrates how to use an SSF format ATHENA file to interpolate doping onto a ATLAS grid and save the doping information for subsequent regrid operations. This is an alternative to the ATHENA/ATLAS interface, which is described in [Section 2.6.1 “Interface From ATHENA”](#).

```
DOPING ATHENA MASTER INFILE=NMOS.DOP OUTFILE=NMOS.DOP  
REGRID DOPING ABS LOG RATIO=4 OUTFILE=NMESSH1.STR  
DOPFILE=NMOS.DOP
```

### 3D Doping Definition Example

The following example illustrates the formation of a Gaussian highly doped n-type area in a three-dimensional structure.

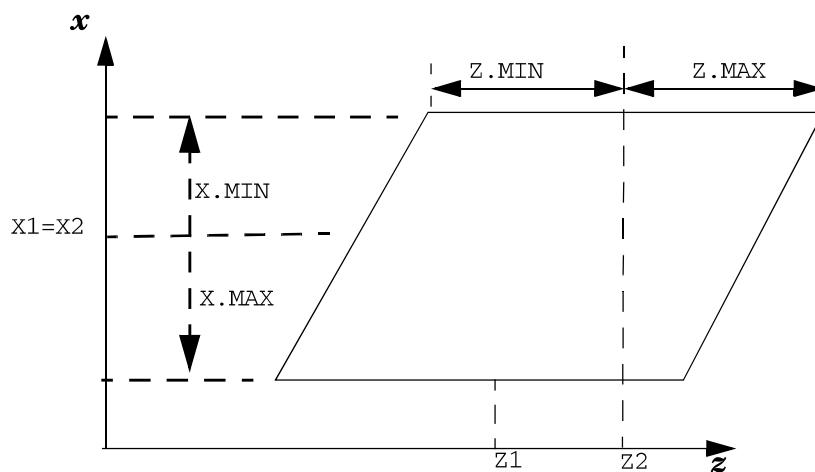
```
DOPING GAUSS N.TYPE CONC=1e20 PEAK=0.0 CHAR=0.2 X.LEFT=0.5 \  
X.RIGHT=1.0 Z.LEFT=0.5 Z.RIGHT=1.0
```

For a cylindrical structure you can use the following syntax. In this case, it is for complementary error function doping.

```
doping erfc start=0.0 char=0.005 ratio.lat=0.1 conc=1.0e20 n.type  
r.min=0.01 a.min=45.0 a.max=225.0
```

### 3D Doping From ASCII 1D File

You can read a 1D doping profile from an ASCII file and apply it to the entire or part of a 3D device. The `X.DIR`, `Y.DIR`, or `Z.DIR` parameters specify the direction of the profile as applied in the 3D device. The starting position of the doping profile will be set by the relevant `X.MIN`, `Y.MIN`, or `Z.MIN` parameter. The ending position of the doping profile will be the minimum of the relevant `X.MIN`, `Y.MIN`, or `Z.MIN` plus the spatial extent of the doping profile in the ASCII file, or the `X.MAX`, `Y.MAX`, `Z.MAX` parameter or a physical boundary of the device. You can specify a general parallelogram in the plane perpendicular to the direction of doping direction. To specify it, use the appropriate combination of `X1`, `X2`, `Y1`, `Y2`, `Z1`, `Z2`, `X.MIN`, `X.MAX`, `Y.MIN`, `Y.MAX`, `Z.MIN`, `Z.MAX`. For example, we consider the `Y.DIR` parameter specified. We can then specify a parallelogram in the XZ plane as shown in [Figure 21-2](#).



**Figure 21-2: Parallelogram Geometry Example**

In the figure, two sides are parallel to the `Z` axis. `z1` and `z2` specify the `Z` coordinate of the midpoints of these two sides. `Z.MIN` and `Z.MAX` together specify the lengths of the sides, and `Z.MIN` will be negative and equal to  $-Z.MAX$ . (In fact, the positions are evaluated as  $z1+Z.MIN$  and  $z1+Z.MAX$  for one side and  $z2+Z.MIN$  and  $z2+Z.MAX$  for the other. Therefore, having `z1` and `z2` and so on refer to the side midpoint is just a convenient convention.)

You must specify `x1` and `x2` as having the same value, and specify `X.MIN` and `X.MAX` the side lengths the same way as for `Z.MIN` and `Z.MAX`.

Setting `z1` and `z2` to the same value will result in a rectangle. By then changing `x1` and `x2` so they are not equal will result in a parallelogram with sides parallel to the `X` axis. If a different direction of doping variation is defined, then a parallelogram can be set up in the plane perpendicular to it in analogously to the above example.

Outside the specified parallelogram the doping level will be either the value of the last point in the ASCII file, or the value specified by the `BACKDOPE` parameter. A smooth transition of the doping from the value inside the parallelogram to the value outside can be applied elsewhere using the `LAT.CHAR` or `RATIO.LAT` parameters.

<b>x1, x2, y1, y2, z1, z2</b>	By convention, specify the midpoints of the sides making up the parallelogram.
<b>x.min, x.max</b>	Determine the X coordinate of the start and end points of the placement of the doping profile read in from an ASCII file (if you specify x.dir). Otherwise, they specify the lateral extent of the parallelogram sides defining the location of the doping in a plane perpendicular to the specified direction of the doping variation. In this case, they are added to x1 and to x2 to determine the coordinates of the ends of sides.
<b>y.min, y.max, z.min, z.max</b>	These are the same as x.min and x.max except they apply to the y and Z directions respectively.

**Example:**

```
doping ascii inf=ydop.dat y.dir n.type x1=6.0 x2=4.0 x.min=-2
x.max=2
z.min=3.0 z.max=7.0 y.min=2.0 y.max=10.0 lat.char=0.005
backdope=0.0
```

This will apply the doping profile specified in ydop.dat as n-type doping in the Y direction between the positions y=2 microns and y=10 microns (unless the length range in ydop.dat is less than this distance). In the XZ plane, it will be applied to a parallelogram with sides parallel to the X direction of length 4 microns. The Z coordinates of these sides are 3.0 microns and 7.0 microns. The doping will transition from the value inside the parallelogram to 0.0 outside on a length scale of 0.005 microns.

**3D Doping From 2D ATHENA Master Files**

In a 2D ATHENA master file, the doping profile is defined over a box in two dimensions. This doping is put over 2D-sections normal to the plane of a parallelogram to be defined in the doping statement. This parallelogram must lie in one of the XY, YZ, and XZ planes and have two edges parallel to one of the coordinate axes.

As the mesh in the ATHENA master file doesn't necessarily coincide with the three-dimensional mesh in ATLAS, an interpolation routine is required to import the doping in ATLAS. You can then choose between a linear and a logarithmic interpolation algorithm.

Here's a list of the parameters that are used for this kind of doping.

<b>ASPECT.RATIO</b>	Specifies the aspect ratio of the doping will be preserved when loaded into the doping parallelogram.
<b>DOP.XMAX</b>	Specifies the maximum X coordinate of the doping in the ATHENA file to be loaded into the doping parallelogram.
<b>DOP.XMIN</b>	Specifies the minimum X coordinate of the doping in the ATHENA file to be loaded into the doping parallelogram.
<b>DOP.YMAX</b>	Specifies the maximum Y coordinate of the doping in the ATHENA file to be loaded into the doping parallelogram.

<b>DOP.YMIN</b>	Specifies the minimum Y coordinate of the doping in the ATHENA file to be loaded into the doping parallelogram.
<b>INT.LIN</b>	Specifies that a linear interpolation is to be used to import doping from ATHENA into ATLAS.
<b>INT.LOG</b>	Specifies that the ATHENA doping is imported in ATLAS by using a logarithmic interpolation algorithm.
<b>INT.OPTM</b>	Enables an optimized interpolation routine, which attempts to reduce CPU time due to the doping interpolation.
<b>LAT.CHAR</b>	Defines the characteristic length, CL, of the lateral spreading (in the $y > y_2$ and $y < y_1$ planes). If RATIO.LAT is used instead, then the characteristic length is assumed to come from this parameter by the height of the parallelogram (i.e., $CL = RL \times OCL$ , OCL being the height of the parallelogram ( $y_2 - y_1$ in this case)). If both LAT.CHAR and RATIO.LAT aren't specified, then no lateral spreading is done.
<b>XY</b>	Specifies that the parallelogram containing doping in ATLAS3D is in the xy plane.
<b>YX</b>	This is a synonym for XY.
<b>YZ</b>	Specifies that a parallelogram containing doping in ATLAS3D is in the YZ plane.
<b>ZY</b>	This is a synonym for YZ.
<b>XZ</b>	Specifies that a parallelogram containing doping in ATLAS3D is in the XZ plane.
<b>ZX</b>	This is a synonym for XZ.
<b>X1, X2, Y1, Y2, Z1, Z2</b>	Specify an average segment in one of the three coordinate planes defining the orientation of the parallelogram.
<b>X.DIR, Y.DIR, Z.DIR</b>	Specify that a parallelogram containing doping in ATLAS3D has two edges in the X direction, Y direction, and Z direction.
<b>X.FLIP</b>	Specifies that the orientation of the ATHENA file X axis will be flipped.
<b>X.MIN, X.MAX</b>	Define the minimum and maximum lateral extent of a parallelogram along the X direction lying in the xy or zx plane, starting from its average segment (they must be specified with x1 and x2). If a parallelogram is defined in the YZ plane, X.MIN can then be used to specify the initial coordinate to start the doping along the X direction.
<b>X.SCALE</b>	Specifies that the ATHENA file doping will be scaled in the X direction.
<b>Y.FLIP</b>	Specifies that the orientation of the ATHENA file Y axis will be flipped.

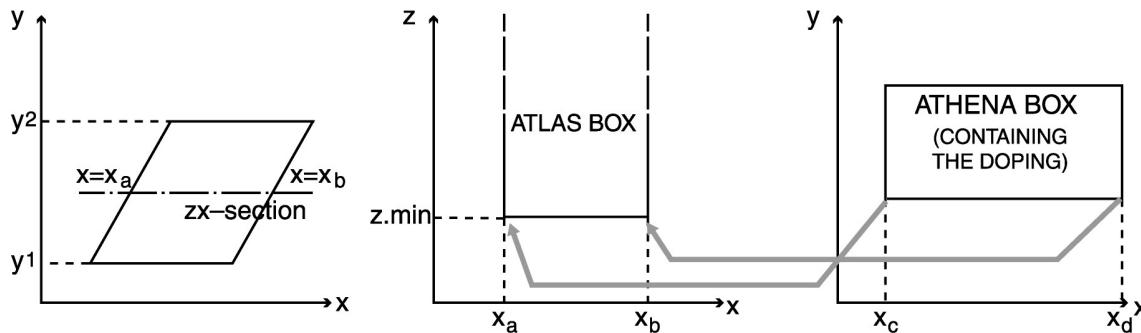
<b>Y.MIN, Y.MAX</b>	Define the minimum and maximum lateral extent of a parallelogram along the Y direction lying in the XY or YZ plane, starting from its average segment (they must be specified with y1 and y2). If a parallelogram is defined in the zx plane, Y.MIN can then be used to specify the initial coordinate to start the doping along the Y direction.
<b>Y.SCALE</b>	Specifies that the ATHENA file doping will be scaled in the Y direction.
<b>Z.MIN, Z.MAX</b>	Define the minimum and maximum lateral extent of a parallelogram along the Z direction lying in the yz or zx plane, starting from its average segment (they must be specified with z1 and z2). If a parallelogram is defined in the xy plane, Z.MIN can then be used to specify the initial coordinate to start the doping along the Z direction.
<b>Z.SCALE</b>	Specifies that the ATHENA file doping will be scaled in the Z direction.

The following three cases, which correspond to the parallelograms in the xy, yz and zx planes, describe how the doping from the ATHENA master file is put into the ATLAS structure .

### First Case: Parallelogram In The XY Plane

SUB-CASE A: Parallelogram along the X direction.

Sections of the ATLAS structure in zx planes are considered, which intersect for  $y1 < y < y2$ , the segment ( $x_a, x_b$ ) inside the parallelogram. Each of these sections defines a box where the 2D doping is imported from ATHENA. Particularly, all the coordinates in ATHENA are scaled and translated so that the edge ( $x_c, x_d$ ) of the ATHENA box containing the doping coincide with the segment ( $x_a, x_b$ ) of the ATLAS box. This is done for all the sections inside the parallelogram. See [Figure 21-3](#).



**Figure 21-3: Parallelogram in the XY plane in the X direction and doping from the ATHENA2D master file**

#### Examples:

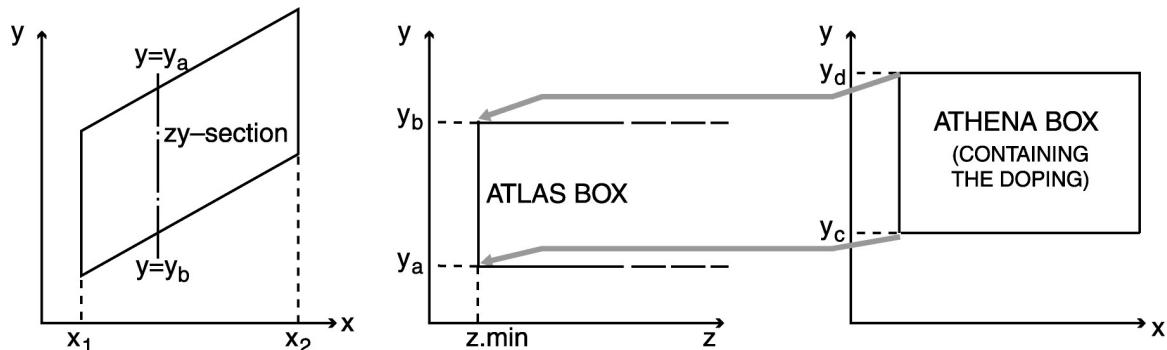
```
doping athena master inf=athena.str boron xy \
x1=2.0 x2=3.0 y1=1.5 y2=4.0 x.dir \
x.min=-2.0 x.max=1.0 z.min=0.6 lat.char=0.05 int.log int.optm
```

For the Z coordinate,  $z.min$  is used to specify the minimum value where to start putting the doping into the zx-sections (which properly defines the segment ( $x_a, x_b$ ) in this plane).

In addition, a lateral spreading can be partially accomplished by extending the parallelogram into the planes,  $y > y_2$  and  $y < y_1$ , where the doping is spread out according to a Gaussian law.

#### SUB-CASE B: Parallelogram along the Y direction

Sections of the ATLAS structure are considered in the YZ planes. A transformation of coordinates in ATHENA is accomplished in order to place the ATHENA segment ( $y_c, y_d$ ) into the ATLAS one ( $y_a, y_b$ ). See [Figure 21-4](#).



**Figure 21-4: Parallelogram in the XY plane in the Y direction and doping from the ATHENA2D master file**

#### Examples:

```
doping athena master inf=athena.str boron xy \
x1=2.0 x2=3.0 y1=1.5 y2=4.0 y.dir \
y.min=-2.0 y.max=1.0 z.min=0.6 lat.char=0.05 int.lin int.optm
```

#### Second Case: YZ Plane

The YZ plane containing the parallelogram is defined by the `yz` parameter (or `zy`) in the DOPING statement.

If parallelograms along the Z direction are defined (specify `Z.DIR` in doping statement), the doping from ATHENA is put over sections in the zx planes. If the parallelograms along the Y direction are defined (using `Y.DIR` in DOPING statement), the doping from ATHENA is put over sections in the xy planes.

The minimum X coordinate in ATLAS to start adding doping can be specified by `X.MIN` in DOPING statement.

#### Examples:

```
doping athena master inf=athena.str boron zy z.dir \
z1=0.3 z2=0.6 y1=0.35 y2=0.25 z.min=-0.2 z.max=0.6 \
x.min=0.2 ratio.lat=0.05
```

```
doping athena master inf=athena.str boron zy y.dir \
z1=0.3 z2=0.6 y1=0.35 y2=0.25 y.min=-0.2 y.max=0.6 \
x.min=0.2 ratio.lat=0.05
```

**Third Case: ZX Plane**

The ZX plane containing the parallelogram is defined by the `zx` parameter (or `xz`) in DOPING statement. If parallelograms along the Z direction are defined (using `z.DIR` in the DOPING statement), the doping from ATHENA is placed over sections in the YZ planes.

If the parallelograms along the X direction are defined (using `x.DIR` in DOPING statement), the doping from ATHENA is placed over the sections in the XY planes.

The minimum Y coordinate in ATLAS to start adding doping can be specified by `y.MIN` in doping statement.

**Examples:**

```
doping athena master inf=athena.str boron int.lin \
xz z.dir z1=0.45 z2=0.55 x1=0.2 x2=0.7 x.min=-0.4 \
x.max=0.2 y.min=0.0 lat.char=0.02
doping athena master inf=athena.str boron int.lin \
xz x.dir z1=0.4 z2=0.8 x1=0.2 x2=0.7 z.min=-0.4 \
z.max=0.2 y.min=0.5 ratio.lat=0.5
```